

## SEQUENCE LISTING

<110> Large Scale Biology Corporation  
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<120> PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT EXPRESSION

<130> LSBC-0087-CP07B

<150> 09/993,059

<151> 2001-11-13

<150> 09/626,127

<151> 2000-07-26

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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg  
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Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser  
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Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp  
65 70 75 80

Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala  
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Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe  
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Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu  
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Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe  
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Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp  
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Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu  
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Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg  
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Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp  
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Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His  
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Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser  
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Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala  
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Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe  
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Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro  
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
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Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
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Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
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Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
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Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
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Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala		
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Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser		
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Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn		
180	185	190
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met		
195	200	205
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn		
210	215	220
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys		
225	230	235
240		
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val		
245	250	255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn		
260	265	270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala		
275	280	285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser		
290	295	300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn		
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Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn		
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Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
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Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
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Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
          35              40              45

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Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
          50              55              60

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Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
65              70              75              80

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Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
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Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
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Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu  
115 120 125

Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe  
130 135 140

Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp  
145 150 155 160

Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu  
165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg  
180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp  
195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His  
210 215 220

Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser  
225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala  
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Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe  
260 265 270

Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile  
275 280 285

Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro  
290 295 300

Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln  
305 310 315 320

Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe  
325 330 335

Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met  
 340 345 350

Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val  
 355 360 365

Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr  
 370 375 380

Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser  
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
          20           25           30

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Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
          35           40           45

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Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
          50           55           60

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Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65           70           75           80

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Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
          85           90           95

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Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
          100          105          110

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Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
          115          120          125

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Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
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 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser  
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn  
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met  
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys  
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val  
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn  
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala  
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser  
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn  
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
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 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420  
 acctgcgcag gcttccttgg gagttttgga tactacgaca ttgatgcca gacctttgct 480  
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<210> 12  
<211> 421  
<212> PRT  
<213> Homo sapiens

<400> 12

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu  
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu  
20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly  
65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met  
85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg  
100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly  
115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala  
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser  
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn  
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met  
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys  
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val  
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn  
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala  
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser  
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn  
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile



370

375

380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
 405 410 415

Leu Glu Asn Thr Met  
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 <211> 1284  
 <212> DNA  
 <213> Homo sapiens

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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180  
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctcagaaggc 240  
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 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360  
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420  
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 tcctgtgagt ggctcttta tatgtggccc tttcaaaagc ccaattatac agaaatccga 660  
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<210> 14  
 <211> 427  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu  
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu  
 20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly  
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met  
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg  
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly  
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
 130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala  
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser

	165		170		175
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	180		185		190
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	195		200		205
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	210		215		220
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys	225		230		235
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val		245		250	255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn		260		265	270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala		275		280	285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser		290		295	300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn		305		310	315
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn		325		330	335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala		340		345	350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala		355		360	365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile		370		375	380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr		385		390	395
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Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
405 410 415

Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu  
420 425

<210> 15  
<211> 1254  
<212> DNA  
<213> Homo sapiens

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accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180  
gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctcagaaggc 240  
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gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360  
gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420  
acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgcca gacctttgct 480  
gactggggag tagatctgct aaaatttgat ggttggttact gtgacagttt ggaaaatttg 540  
gcagatgggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600  
tcctgtgagt ggccctcttta tatgtggccc tttcaaaagc ccaattatac agaaatccga 660  
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<210> 16  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu  
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu  
 20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly  
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met  
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg  
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly  
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
 130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala  
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser  
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn  
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met  
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys  
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val  
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn  
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala  
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser  
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn  
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
 405 410 415

Leu

<210> 17  
 <211> 1272  
 <212> DNA  
 <213> Homo sapiens

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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180  
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctgagaaggc 240  
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 gattcagaag gcagacttca ggcagacct cagcgctttc ctcatgggat tcgccagcta 360  
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 acctgcgcag gcttccttgg gagttttgga tactacgaca ttgatgcca gacctttgct 480  
 gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540  
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600  
 tcctgtgagt ggctcttcta tatgtggccc ttcaaaagc ccaattatac agaaatccga 660  
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720  
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780  
 gggttgaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840  
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 gacgaattat ga 1272

<210> 18  
 <211> 423  
 <212> PRT

<213> Homo sapiens

<400> 18

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu  
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu  
20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly  
65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met  
85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg  
100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly  
115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala  
145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser  
165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn  
180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met  
195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn





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<212> DNA
<213> Homo sapiens

<400> 19
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accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca      180
gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggg ctcagaaggc      240
tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga      300
gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta      360
gctaattatg ttcacagcaa aggactgaag ctagggattht atgcagatgt tggaaataaa      420
acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgcccc gacctttgct      480
gactggggag tagatctgct aaaatttgat gggtgttact gtgacagttt ggaaaatttg      540
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tcctgtgagt ggccctctta tatgtggccc ttcaaaaagc ccaattatac agaaatccga      660
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caggacccct tgggcaagca agggtagcag cttagacagg gagacaactt tgaagtgtgg     1020
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ggacctcgct cttataccat cgcagttgct tcctgggta aaggagtggc ctgtaatect     1140
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tcaagggttaa gataa                                                         1215

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<210> 20
<211> 401
<212> PRT
<213> Homo sapiens

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<400> 20

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1          5          10          15

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Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly  
                   20                  25                  30

Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met  
                   35                  40                  45

Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys  
           50                  55                  60

Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp Lys Asp  
 65                  70                  75                  80

Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala Pro Gln  
                   85                  90                  95

Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe Pro His  
                   100                  105                  110

Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys Leu  
                   115                  120                  125

Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly  
           130                  135                  140

Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly  
 145                  150                  155                  160

Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn  
                   165                  170                  175

Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg Thr Gly  
                   180                  185                  190

Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp Pro Phe  
           195                  200                  205

Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His Trp Arg  
           210                  215                  220

Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu  
 225                  230                  235                  240

Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro  
245 250 255

Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu  
260 265 270

Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala  
275 280 285

Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro Gln Ala  
290 295 300

Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln Asp Pro  
305 310 315 320

Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe Glu Val  
325 330 335

Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn  
340 345 350

Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser  
355 360 365

Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu  
370 375 380

Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu  
385 390 395 400

Arg

<210> 21  
<211> 1233  
<212> DNA  
<213> Homo sapiens

<400> 21  
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accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180  
gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggg ctcagaaggc 240

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gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa    420
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gcagatgggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac    600
tcctgtgagt ggctcttcta tatgtggccc tttcaaaagc ccaattatac agaaatccga    660
cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag    720
agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg    780
ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa    840
gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc    900
cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat    960
caggaccctt tgggcaagca agggtagcag cttagacagg gagacaactt tgaagtgtgg   1020
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gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact   1200
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<210> 22
<211> 409
<212> PRT
<213> Homo sapiens

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<400> 22
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Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg
1           5           10           15

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Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp
20           25           30

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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
35           40           45

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Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
50           55           60

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Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp  
 65 70 75 80

Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala  
 85 90 95

Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe  
 100 105 110

Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu  
 115 120 125

Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe  
 130 135 140

Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp  
 145 150 155 160

Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu  
 165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg  
 180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp  
 195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His  
 210 215 220

Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser  
 225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala  
 245 250 255

Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe  
 260 265 270

Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile  
 275 280 285

Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro  
 290 295 300

Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln  
 305 310 315 320

Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe  
 325 330 335

Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met  
 340 345 350

Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val  
 355 360 365

Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr  
 370 375 380

Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser  
 385 390 395 400

Arg Leu Arg Ser Glu Lys Asp Glu Leu  
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<210> 23  
 <211> 30  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 23

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
 1 5 10 15

Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu  
 20 25 30

<210> 24  
 <211> 36  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 24

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
 1 5 10 15

Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu Ser Glu  
 20 25 30

Lys Asp Glu Leu  
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<210> 25  
 <211> 26  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 25

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
 1 5 10 15

Gln Leu Glu Asn Thr Met Gln Met Ser Leu  
 20 25

<210> 26  
 <211> 32  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 26

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
 1 5 10 15

Gln Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu  
 20 25 30

<210> 27  
 <211> 22  
 <212> PRT  
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<400> 27

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
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Gln Leu Glu Asn Thr Met  
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<210> 28  
 <211> 29



<212> PRT  
<213> Tobacco mosaic virus

<400> 28

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Thr Val Leu  
1 5 10 15

Leu Gln Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu  
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<210> 29  
<211> 18  
<212> PRT  
<213> Tobacco mosaic virus

<400> 29

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
1 5 10 15

Gln Leu

<210> 30  
<211> 24  
<212> PRT  
<213> Tobacco mosaic virus

<400> 30

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1 5 10 15

Gln Leu Ser Glu Lys Asp Glu Leu  
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<210> 31  
<211> 5  
<212> PRT  
<213> Tobacco mosaic virus

<400> 31

Thr Ser Arg Leu Arg  
1 5

<210> 32  
<211> 11  
<212> PRT

<213> Tobacco mosaic virus

<400> 32

Thr	Ser	Arg	Leu	Arg	Ser	Glu	Lys	Asp	Glu	Leu
1				5					10	